

RAW SEQUENCE LISTING

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Application Serial Number: 10/506,448A
Source: PCT/10
Date Processed by STIC: 6/15/05

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PCT

RAW SEQUENCE LISTING

DATE: 06/15/2005

PATENT APPLICATION: US/10/506,448A

TIME: 15:52:03

Input Set : A:\SEQUENCE LISTING.ST25.txt

Output Set: N:\CRF4\06152005\J506448A.raw

3 <110> APPLICANT: Plantechno S.r.l.
4 Plantechno S.r.l.
6 <120> TITLE OF INVENTION: IN-SEED LYSOSOMAL ENZYMES
8 <130> FILE REFERENCE: BW266R/RVP/rmp
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/506,448A
C--> 10 <141> CURRENT FILING DATE: 2004-09-01
10 <150> PRIOR APPLICATION NUMBER: RM2002A000115
11 <151> PRIOR FILING DATE: 2002-01-03
13 <160> NUMBER OF SEQ ID NOS: 15
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1551
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: sig_peptide
24 <222> LOCATION: (1)..(57)
25 <223> OTHER INFORMATION:
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1548)
30 <223> OTHER INFORMATION:

W--> 32 <220>
33 <221> NAME/KEY: mat_peptide
34 <222> LOCATION: (58)..()
35 <223> OTHER INFORMATION:

W--> 37 <400> 1

38	atg	gct	ggc	agc	ctc	aca	ggt	ttg	ctt	cta	ctt	cag	gca	gtg	tcg	tgg	48
39	Met	Ala	Gly	Ser	Leu	Thr	Gly	Leu	Leu	Leu	Leu	Gln	Ala	Val	Ser	Trp	
40					-15					-10					-5		
42	gca	tca	ggg	gcc	cgc	ccc	tgc	atc	cct	aaa	agc	ttc	ggc	tac	agc	tcg	96
43	Ala	Ser	Gly	Ala	Arg	Pro	Cys	Ile	Pro	Lys	Ser	Phe	Gly	Tyr	Ser	Ser	
44					-1	1			5					10			
46	gtg	gtg	tgt	gtc	tgc	aat	gcc	aca	tac	tgt	gac	tcc	ttt	gac	ccc	ccg	144
47	Val	Val	Cys	Val	Cys	Asn	Ala	Thr	Tyr	Cys	Asp	Ser	Phe	Asp	Pro	Pro	
48					15				20				25				
50	acc	ttt	cct	gcc	ctt	ggt	acc	ttc	agc	cgc	tat	gag	agt	aca	cgc	agt	192
51	Thr	Phe	Pro	Ala	Leu	Gly	Thr	Phe	Ser	Arg	Tyr	Glu	Ser	Thr	Arg	Ser	
52	30					35				40				45			
54	ggg	cga	cgg	atg	gag	ctg	agt	atg	ggg	ccc	atc	cag	gct	aat	cac	acg	240
55	Gly	Arg	Arg	Met	Glu	Leu	Ser	Met	Gly	Pro	Ile	Gln	Ala	Asn	His	Thr	
56						50				55				60			
58	qgc	aca	qgc	ctg	cta	ctg	acc	ctg	caq	cca	qaa	caq	aag	ttc	caq	aaa	288

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59	Gly	Thr	Gly	Leu	Leu	Leu	Thr	Leu	Gln	Pro	Glu	Gln	Lys	Phe	Gln	Lys
60				65				70					75			
62	gtg	aag	gga	ttt	gga	ggg	gcc	atg	aca	aat	tgc	gct	gtc	ctc	aac	atc
63	Val	Lys	Gly	Phe	Gly	Gly	Ala	Met	Thr	Asp	Ala	Ala	Ala	Leu	Asn	Ile
64				80				85					90			
66	ctt	gcc	ctg	tca	ccc	cct	gcc	caa	aat	ttg	cta	ctt	aaa	tcg	tac	tcc
67	Leu	Ala	Leu	Ser	Pro	Pro	Ala	Gln	Asn	Leu	Leu	Leu	Lys	Ser	Tyr	Phe
68					95			100					105			
70	tct	gaa	gaa	gga	atc	gga	tat	aac	atc	atc	cg	gta	ccc	atg	gcc	agc
71	Ser	Glu	Glu	Gly	Ile	Gly	Tyr	Asn	Ile	Ile	Arg	Val	Pro	Met	Ala	Ser
72	110					115					120					125
74	tgt	gac	ttc	tcc	atc	cgc	acc	tac	acc	tat	gca	gac	acc	cct	gat	gat
75	Cys	Asp	Phe	Ser	Ile	Arg	Thr	Tyr	Thr	Tyr	Ala	Asp	Thr	Pro	Asp	Asp
76						130				135					140	
78	ttc	cag	ttg	cac	aac	ttc	agc	ctc	cca	gag	gaa	gat	acc	aag	ctc	aag
79	Phe	Gln	Leu	His	Asn	Phe	Ser	Leu	Pro	Glu	Glu	Asp	Thr	Lys	Leu	Lys
80					145				150				155			
82	ata	ccc	ctg	att	cac	cga	gcc	ctg	cag	ttg	gcc	cag	cgt	ccc	gtt	tca
83	Ile	Pro	Leu	Ile	His	Arg	Ala	Leu	Gln	Leu	Ala	Gln	Arg	Pro	Val	Ser
84					160			165					170			
86	ctc	ctt	gcc	agc	ccc	tgg	aca	tca	ccc	act	tgg	ctc	aag	acc	aat	gga
87	Leu	Leu	Ala	Ser	Pro	Trp	Thr	Ser	Pro	Thr	Trp	Leu	Lys	Thr	Asn	Gly
88					175			180				185				
90	gcg	gtg	aat	ggg	aag	ggg	tca	ctc	aag	gga	cag	ccc	gga	gac	atc	tac
91	Ala	Val	Asn	Gly	Lys	Gly	Ser	Leu	Lys	Gly	Gln	Pro	Gly	Asp	Ile	Tyr
92	190					195				200				205		
94	cac	cag	acc	tgg	gcc	aga	tac	ttt	gtg	aag	ttc	ctg	gat	gcc	tat	gct
95	His	Gln	Thr	Trp	Ala	Arg	Tyr	Phe	Val	Lys	Phe	Leu	Asp	Ala	Tyr	Ala
96					210				215				220			
98	gag	cac	aag	tta	cag	ttc	tgg	gca	gtg	aca	gct	gaa	aat	gag	cct	tct
99	Glu	His	Lys	Leu	Gln	Phe	Trp	Ala	Val	Thr	Ala	Glu	Asn	Glu	Pro	Ser
100					225				230				235			
102	gct	ggg	ctg	ttg	agt	gga	tac	ccc	ttc	cag	tgc	ggc	ttc	acc	cct	
103	Ala	Gly	Leu	Leu	Ser	Gly	Tyr	Pro	Phe	Gln	Cys	Leu	Gly	Phe	Thr	Pro
104					240			245				250				
106	gaa	cat	cag	cga	gac	ttc	att	gcc	cgt	gac	cta	ggt	cct	acc	ctc	gcc
107	Glu	His	Gln	Arg	Asp	Phe	Ile	Ala	Arg	Asp	Leu	Gly	Pro	Thr	Leu	Ala
108					255			260				265				
110	aac	agt	act	cac	cac	aat	gtc	cgc	cta	ctc	atg	ctg	gat	gac	caa	cgc
111	Asn	Ser	Thr	His	His	Asn	Val	Arg	Leu	Leu	Met	Leu	Asp	Asp	Gln	Arg
112	270					275				280				285		
114	ttg	ctg	ctg	ccc	cac	tgg	gca	aag	gtg	gta	ctg	aca	gac	cca	gaa	gca
115	Leu	Leu	Leu	Pro	His	Trp	Ala	Lys	Val	Val	Leu	Thr	Asp	Pro	Glu	Ala
116						290			295				300			
118	gct	aaa	tat	gtt	cat	ggc	att	gct	gta	cat	tgg	tac	ctg	gac	ttt	ctg
119	Ala	Lys	Tyr	Val	His	Gly	Ile	Ala	Val	His	Trp	Tyr	Leu	Asp	Phe	Leu
120					305				310				315			
122	gct	cca	gcc	aaa	gcc	acc	cta	ggg	gag	aca	cac	cgc	ctg	ttc	ccc	aac
123	Ala	Pro	Ala	Lys	Ala	Thr	Leu	Gly	Glu	Thr	His	Arg	Leu	Phe	Pro	Asn

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124	320	325	330	
126	acc atg ctc ttt gcc tca gag gcc tgt gtg ggc tcc aag ttc tgg gag			1104
127	Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu			
128	335	340	345	
130	cag agt gtg cgg cta ggc tcc tgg gat cga ggg atg cag tac agc cac			1152
131	Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His			
132	350	355	360	365
134	agc atc atc acg aac ctc ctg tac cat gtg gtc ggc tgg acc gac tgg			1200
135	Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp			
136	370	375	380	
138	aac ctt gcc ctg aac ccc gaa gga gga ccc aat tgg gtg cgt aac ttt			1248
139	Asn Leu Ala Leu Asn Pro Glu Gly Pro Asn Trp Val Arg Asn Phe			
140	385	390	395	
142	gtc gac agt ccc atc att gta gac atc acc aag gac acg ttt tac aaa			1296
143	Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys			
144	400	405	410	
146	cag ccc atg ttc tac cac ctt ggc cac ttc agc aag ttc att cct gag			1344
147	Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu			
148	415	420	425	
150	ggc tcc cag aga gtg ggg ctg gtt gcc agt cag aag aac gac ctg gac			1392
151	Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp			
152	430	435	440	445
154	gca gtg gca ctg atg cat ccc gat ggc tct gct gtt gtg gtc gtg cta			1440
155	Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Leu			
156	450	455	460	
158	aac cgc tcc tct aag gat gtg cct ctt acc atc aag gat cct gct gtg			1488
159	Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val			
160	465	470	475	
162	ggc ttc ctg gag aca atc tca cct ggc tac tcc att cac acc tac ctg			1536
163	Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu			
164	480	485	490	
166	tgg cat cgc cag tga			1551
167	Trp His Arg Gln			
168	495			
171	<210> SEQ ID NO: 2			
172	<211> LENGTH: 516			
173	<212> TYPE: PRT			
174	<213> ORGANISM: Homo sapiens			
176	<400> SEQUENCE: 2			
178	Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Gln Ala Val Ser Trp			
179	-15	-10	-5	
182	Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser			
183	-1 1	5	10	
186	Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro			
187	15	20	25	
190	Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser			
191	30	35	40	45
194	Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr			
195	50	55	60	

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198 Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys
 199 65 70 75
 202 Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile
 203 80 85 90
 206 Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe
 207 95 100 105
 210 Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser
 211 110 115 120 125
 214 Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp
 215 130 135 140
 218 Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys
 219 145 150 155
 222 Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser
 223 160 165 170
 226 Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly
 227 175 180 185
 230 Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr
 231 190 195 200 205
 234 His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala
 235 210 215 220
 238 Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser
 239 225 230 235
 242 Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro
 243 240 245 250
 246 Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala
 247 255 260 265
 250 Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg
 251 270 275 280 285
 254 Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala
 255 290 295 300
 258 Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu
 259 305 310 315
 262 Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn
 263 320 325 330
 266 Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu
 267 335 340 345
 270 Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His
 271 350 355 360 365
 274 Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp
 275 370 375 380
 278 Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe
 279 385 390 395
 282 Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys
 283 400 405 410
 286 Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu
 287 415 420 425
 290 Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp
 291 430 435 440 445
 294 Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Leu

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295	450	455	460
298	Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val		
299	465	470	475
302	Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu		
303	480	485	490
306	Trp His Arg Gln		
307	495		
310	<210> SEQ ID NO: 3		
311	<211> LENGTH: 27		
312	<212> TYPE: DNA		
313	<213> ORGANISM: Artificial Sequence		
315	<220> FEATURE:		
316	<223> OTHER INFORMATION: forward primer for human GCB amplification including DNA coding f		
317	or native signal peptide		
319	<400> SEQUENCE: 3		
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323	<210> SEQ ID NO: 4		
324	<211> LENGTH: 33		
325	<212> TYPE: DNA		
326	<213> ORGANISM: Artificial Sequence		
328	<220> FEATURE:		
329	<223> OTHER INFORMATION: Reverse primer for human GCB amplification		
331	<400> SEQUENCE: 4		
332	gtgtggatgg acaccgttagc ggtcactctc gag		33
335	<210> SEQ ID NO: 5		
336	<211> LENGTH: 31		
337	<212> TYPE: DNA		
338	<213> ORGANISM: Artificial Sequence		
340	<220> FEATURE:		
341	<223> OTHER INFORMATION: forward primer for human GCB amplification excluding DNA coding f		
342	or native signal peptide		
344	<400> SEQUENCE: 5		
345	cccggttgcc cgccccctgca tccctaaaag c		31
348	<210> SEQ ID NO: 6		
349	<211> LENGTH: 1428		
350	<212> TYPE: DNA		
351	<213> ORGANISM: Glycine max		
353	<220> FEATURE:		
354	<221> NAME/KEY: promoter		
355	<222> LOCATION: (1)..(1428)		
356	<223> OTHER INFORMATION:		
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361	tttttttacc agaaatccgt taatatttgtt aaaatattac caactaattt ataaattttta		120
363	ttttaaggca attaagcatg ttgtataaaa tatatatatt gttataaata cttttcaaaa		180
365	gtataaaagt gatgtatggcg ttgtggtaga ttattttagt tcttaggtcg aatgcaagtt		240
367	gttttagaca tttagcctta ttcttttttc taacaaaaat aaatgtaaat ggaaaacctt		300
369	tagaaaaaaa aagaaatcaa aattgaaaac atcatccggt ggagtcgaga agcccacacc		360
371	cacgtgaccc aacaatatta aaataagagt ttgctctaca gtaaatgcga tacttttta		420

VERIFICATION SUMMARY

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Output Set: N:\CRF4\06152005\J506448A.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
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L:713 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:706
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L:718 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:716